



SEQUENCE LISTING

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Koetting, Oliver
Ritte, Gerhard
Steup, Martin

<120> Plants with increased activity of a starch phosphorylating enzyme

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<151> 2004-03-05

<150> EP04090121.7
<151> 2004-03-29

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gca tcc agg aac tgg tgg cgg aag tta gag gtt gtt cgc ggg ata ttg Ala Ser Arg Asn Trp Trp Arg Lys Leu Glu Val Val Arg Gly Ile Leu 270 275 280 285	867
tca gaa tct ttt gat gac cag agt cgt ctg ggg gcc ctt gta tac tca Ser Glu Ser Phe Asp Asp Gln Ser Arg Leu Gly Ala Leu Val Tyr Ser 290 295 300	915
gct att tat ctg aag tgg att tat aca ggt cag ata tcg tgc ttt gaa Ala Ile Tyr Leu Lys Trp Ile Tyr Thr Gly Gln Ile Ser Cys Phe Glu 305 310 315	963
gat ggt ggc cac cat cgg cct aac aaa cat gct gag ata tcg agg caa Asp Gly Gly His His Arg Pro Asn Lys His Ala Glu Ile Ser Arg Gln 320 325 330	1011
ata ttc cgt gaa ctt gaa atg atg tat tat ggg aaa acc aca tca gcc Ile Phe Arg Glu Leu Glu Met Met Tyr Tyr Gly Lys Thr Thr Ser Ala 335 340 345	1059
aag gat gtt ctc gtg att cgc aaa att cat ccc ttt tta cct tca ttt Lys Asp Val Leu Val Ile Arg Lys Ile His Pro Phe Leu Pro Ser Phe 350 355 360 365	1107
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gct cac cgg aat gac atc cca cat gat ctc aag caa gaa atc aag cat Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys His 385 390 395	1203
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agt Ser 430	gaa Glu	aca Thr	ttt Phe	gtt Val	gaa Glu 435	caa Gln	ttc Phe	acg Thr	ata Ile	ttt Phe 440	tat Tyr	agc Ser	gaa Glu	cta Leu	aaa Lys 445	1347
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gaa Glu	tct Ser	ctg Leu	aac Asn 465	gag Glu	tca Ser	ggc Gly	tta Leu	gaa Glu 470	gtt Val	ctc Leu	tca Ser	tcc Ser	ttt Phe 475	gtg Val	gaa Glu	1443
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aat Asn 495	gat Asp	acc Thr	att Ile	caa Gln	att Ile	ttg Leu 500	atg Met	act Thr	acc Thr	ttg Leu 505	caa Gln	tca Ser	tta Leu	tct Ser	tct Ser	1539
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gcg Ala	cct Pro	gat Asp	aat Asn	gct Ala 530	ata Ile	gca Ala	atg Met	cga Arg	caa Gln 535	aag Lys	tgg Trp	cgc Arg	ctt Leu	tgt Cys 540	gaa Glu	1635
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aga Arg	aat Asn 575	act Thr	act Thr	cta Leu	tgg Trp	gat Asp 580	act Thr	act Thr	ctt Leu	gat Asp	gcc Ala 585	ctt Leu	gtc Val	att Ile	ggc Gly	1779
atc Ile 590	aat Asn	caa Gln	gtt Val	agc Ser	ttt Phe 595	tca Ser	ggc Gly	tgg Trp	aaa Lys	aca Thr 600	gat Asp	gaa Glu	tgt Cys	att Ile	gcc Ala 605	1827
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gaa Glu	ggc Gly	tgt Cys	gaa Glu 625	gat Asp	ggc Gly	aaa Lys	tat Tyr	att Ile 630	tgg Trp	tca Ser	cta Leu	aga Arg	ctt Leu 635	aaa Lys	gct Ala	1923
aca Thr	ctg Leu	gac Asp 640	aga Arg	gca Ala	cgg Arg	aga Arg	tta Leu 645	acg Thr	gaa Glu	gag Glu	tac Tyr	tct Ser 650	gaa Glu	gca Ala	ctt Leu	1971
ctt Leu 655	tct Ser	ata Ile	ttc Phe	cct Pro	gaa Glu 660	aaa Lys	gta Val	atg Met	gtt Val	att Ile	ggc Gly 665	aaa Lys	gcc Ala	ctt Leu	gga Gly	2019

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ggc Gly	att Ile	gtt Val	ttt Phe 690	cag Gln	gta Val	tct Ser	aaa Lys	cta Leu	tgc Cys 695	aca Thr	gta Val	ctt Leu	cag Gln	aaa Lys 700	gca Ala	2115
att Ile	cga Arg	gaa Glu	gta Val 705	ctt Leu	gga Gly	tca Ser	act Thr	ggc Gly 710	tgg Trp	gat Asp	gtt Val	ctt Leu	gtt Val 715	cct Pro	gga Gly	2163
gtg Val	gcc Ala	cat His 720	gga Gly	act Thr	ctg Leu	atg Met	cgg Arg 725	gtg Val	gaa Glu	aga Arg	att Ile	ctt Leu 730	cct Pro	gga Gly	tca Ser	2211
tta Leu	cct Pro 735	tca Ser	tct Ser	gtc Val	aaa Lys	gaa Glu 740	cct Pro	gtg Val	gtt Val	cta Leu	att Ile 745	gta Val	gat Asp	aag Lys	gct Ala	2259
gat Asp 750	gga Gly	gat Asp	gaa Glu	gag Glu	gtc Val 755	aaa Lys	gct Ala	gct Ala	ggg Gly	gat Asp 760	aat Asn	ata Ile	gtt Val	ggt Gly	gtt Val 765	2307
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cgt Arg	caa Gln	gag Glu	aat Asn 785	gtt Val	gta Val	ttt Phe	gta Val	act Thr 790	tgt Cys	gaa Glu	tat Tyr	gat Asp	gac Asp 795	aca Thr	gtt Val	2403
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tcc Ser	atc Ile 815	aat Asn	gtc Val	aat Asn	ctc Leu	tca Ser 820	ata Ile	gtt Val	tca Ser	gaa Glu	aaa Lys 825	aat Asn	gac Asp	aat Asn	gct Ala	2499
gtc Val 830	tct Ser	aca Thr	gaa Glu	cca Pro	aat Asn 835	agt Ser	aca Thr	ggg Gly	aat Asn	cca Pro 840	ttt Phe	caa Gln	cag Gln	aaa Lys	ctc Leu 845	2547
caa Gln	aat Asn	gaa Glu	ttc Phe 850	tct Ser	cta Leu	cca Pro	tcg Ser	gat Asp	atc Ile 855	gag Glu	atg Met	cca Pro	ctg Leu	caa Gln 860	atg Met	2595
tct Ser	aag Lys	caa Gln	aaa Lys 865	agc Ser	aaa Lys	tca Ser	gga Gly	gtg Val 870	aat Asn	ggt Gly	agt Ser	ttt Phe	gct Ala 875	gct Ala	ctt Leu	2643
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tgc Cys	aga Arg 895	act Thr	ctt Leu	tct Ser	gtt Val	ctt Leu 900	gct Ala	tca Ser	ttg Leu	tct Ser	aat Asn 905	aaa Lys	gtc Val	tat Tyr	agt Ser	2739
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cca ttt gga tca atg gag gat gcg ctc aag aaa agt gga tca ctg gaa Pro Phe Gly Ser Met Glu Asp Ala Leu Lys Lys Ser Gly Ser Leu Glu 930 935 940	2835
tcc ttt aca agc ctt cta gaa aag att gaa aca gcc aaa gtc gaa aat Ser Phe Thr Ser Leu Leu Glu Lys Ile Glu Thr Ala Lys Val Glu Asn 945 950 955	2883
ggc gaa gtt gat agc ctg gcg ttg gag cta caa gca ata att tca cat Gly Glu Val Asp Ser Leu Ala Leu Glu Leu Gln Ala Ile Ser His 960 965 970	2931
ctt tcc cca ccg gag gag act att ata ttt ctc aaa aga atc ttc cca Leu Ser Pro Pro Glu Glu Thr Ile Ile Phe Leu Lys Arg Ile Phe Pro 975 980 985	2979
cag gat gtc cgg ttg att gtt aga tct agt gct aat gtg gag gat ttg Gln Asp Val Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu Asp Leu 990 995 1000 1005	3027
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agt ctc atg gac cca tgt gcc ttt gga gct gcg gtt ggg aag gtt Ser Leu Met Asp Pro Cys Ala Phe Gly Ala Ala Val Gly Lys Val 1025 1030 1035	3117
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ccc gct gac cat gac ccc aag gtt gtc cag gct gag gtc gcc cct Pro Ala Asp His Asp Pro Lys Val Val Gln Ala Glu Val Ala Pro 1085 1090 1095	3297
ggg ctg ggt gaa acg ctt gct tca gga acc cgt ggc acc ccg tgg Gly Leu Gly Glu Thr Leu Ala Ser Gly Thr Arg Gly Thr Pro Trp 1100 1105 1110	3342
agg ctg tca tgt aac aaa ttc gat gga aaa gtt gcc act ctt gcc Arg Leu Ser Cys Asn Lys Phe Asp Gly Lys Val Ala Thr Leu Ala 1115 1120 1125	3387
ttt tca aat ttc agt gag gag atg gtg gtg cac aac tct ggt cct Phe Ser Asn Phe Ser Glu Glu Met Val Val His Asn Ser Gly Pro 1130 1135 1140	3432
gcc aat gga gaa gta att cgt ctt act gtt gat tac agc aag aag Ala Asn Gly Glu Val Ile Arg Leu Thr Val Asp Tyr Ser Lys Lys 1145 1150 1155	3477
cca ttg tcg gtt gat aca acc ttt agg aag cag ttt ggt cag cga Pro Leu Ser Val Asp Thr Thr Phe Arg Lys Gln Phe Gly Gln Arg 1160 1165 1170	3522

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 Leu Ala Ala Ile Gly Gln Tyr Leu Glu Gln Lys Phe Gly Ser Ala 1185
 1175 1180

cag gat gtg gaa ggt tgc ctg gtt ggg aaa gat att ttt ata gtg 3612
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Leu Leu Arg Arg Gly Ala Met Ala Leu Pro Gly Arg Arg Gly Phe Ala
 35 40 45

Cys Arg Gly Arg Ser Ala Ala Ser Ala Ala Glu Arg Thr Lys Glu Lys
 50 55 60

Lys Arg Arg Asp Ser Ser Lys Gln Pro Leu Val His Leu Gln Val Cys
 65 70 75 80

Leu Glu His Gln Val Lys Phe Gly Glu His Val Gly Ile Ile Gly Ser
 85 90 95

Thr Lys Glu Leu Gly Ser Trp Glu Glu Gln Val Glu Leu Glu Trp Thr
 100 105 110

Thr Asn Gly Trp Val Cys Gln Leu Lys Leu Pro Gly Glu Thr Leu Val
 115 120 125

Glu Phe Lys Phe Val Ile Phe Leu Val Gly Gly Lys Asp Lys Ile Trp
 130 135 140

Glu Asp Gly Asn Asn Arg Val Val Glu Leu Pro Lys Asp Gly Lys Phe
 145 150 155 160

Asp Ile Val Cys His Trp Asn Arg Thr Glu Glu Pro Leu Glu Leu Leu
 165 170 175

Gly Thr Pro Lys Phe Glu Leu Val Gly Glu Ala Glu Lys Asn Thr Gly
 180 185 190
 Glu Asp Ala Ser Ala Ser Val Thr Phe Ala Pro Glu Lys Val Gln Asp
 195 200 205
 Ile Ser Val Val Glu Asn Gly Asp Pro Ala Pro Glu Ala Glu Ser Ser
 210 215 220
 Lys Phe Gly Gly Gln Trp Gln Gly Ser Lys Thr Val Phe Met Arg Ser
 225 230 235 240
 Asn Glu His Leu Asn Lys Glu Ala Asp Arg Met Trp Asp Thr Thr Gly
 245 250 255
 Leu Asp Gly Ile Ala Leu Lys Leu Val Glu Gly Asp Lys Ala Ser Arg
 260 265 270
 Asn Trp Trp Arg Lys Leu Glu Val Val Arg Gly Ile Leu Ser Glu Ser
 275 280 285
 Phe Asp Asp Gln Ser Arg Leu Gly Ala Leu Val Tyr Ser Ala Ile Tyr
 290 295 300
 Leu Lys Trp Ile Tyr Thr Gly Gln Ile Ser Cys Phe Glu Asp Gly Gly
 305 310 315 320
 His His Arg Pro Asn Lys His Ala Glu Ile Ser Arg Gln Ile Phe Arg
 325 330 335
 Glu Leu Glu Met Met Tyr Tyr Gly Lys Thr Thr Ser Ala Lys Asp Val
 340 345 350
 Leu Val Ile Arg Lys Ile His Pro Phe Leu Pro Ser Phe Lys Ser Glu
 355 360 365
 Phe Thr Ala Ser Val Pro Leu Thr Arg Ile Arg Asp Ile Ala His Arg
 370 375 380
 Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys His Thr Ile Gln
 385 390 395 400
 Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu Ile Ala Thr Glu
 405 410 415
 Val Met Leu Ala Arg Ile Thr Lys Thr Pro Gly Glu Tyr Ser Glu Thr
 420 425 430

Phe Val Glu Gln Phe Thr Ile Phe Tyr Ser Glu Leu Lys Asp Phe Phe
 435 440 445

Asn Ala Gly Ser Leu Phe Glu Gln Leu Glu Ser Ile Lys Glu Ser Leu
 450 455 460

Asn Glu Ser Gly Leu Glu Val Leu Ser Ser Phe Val Glu Thr Lys Arg
 465 470 475 480

Ser Leu Asp Gln Val Asp His Ala Glu Asp Leu Asp Lys Asn Asp Thr
 485 490 495

Ile Gln Ile Leu Met Thr Thr Leu Gln Ser Leu Ser Ser Leu Arg Ser
 500 505 510

Val Leu Met Lys Gly Leu Glu Ser Gly Leu Arg Asn Asp Ala Pro Asp
 515 520 525

Asn Ala Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Ser Leu
 530 535 540

Glu Asp Tyr Ser Phe Val Leu Leu Ser Arg Phe Ile Asn Thr Leu Glu
 545 550 555 560

Ala Leu Gly Gly Ser Ala Ser Leu Ala Lys Asp Val Ala Arg Asn Thr
 565 570 575

Thr Leu Trp Asp Thr Thr Leu Asp Ala Leu Val Ile Gly Ile Asn Gln
 580 585 590

Val Ser Phe Ser Gly Trp Lys Thr Asp Glu Cys Ile Ala Ile Gly Asn
 595 600 605

Glu Ile Leu Ser Trp Lys Gln Lys Gly Leu Ser Glu Ser Glu Gly Cys
 610 615 620

Glu Asp Gly Lys Tyr Ile Trp Ser Leu Arg Leu Lys Ala Thr Leu Asp
 625 630 635 640

Arg Ala Arg Arg Leu Thr Glu Glu Tyr Ser Glu Ala Leu Leu Ser Ile
 645 650 655

Phe Pro Glu Lys Val Met Val Ile Gly Lys Ala Leu Gly Ile Pro Asp
 660 665 670

Asn Ser Val Arg Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Val
 675 680 685

Phe Gln Val Ser Lys Leu Cys Thr Val Leu Gln Lys Ala Ile Arg Glu
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 Val Leu Gly Ser Thr Gly Trp Asp Val Leu Val Pro Gly Val Ala His
 705 710 715 720
 Gly Thr Leu Met Arg Val Glu Arg Ile Leu Pro Gly Ser Leu Pro Ser
 725 730 735
 Ser Val Lys Glu Pro Val Val Leu Ile Val Asp Lys Ala Asp Gly Asp
 740 745 750
 Glu Glu Val Lys Ala Ala Gly Asp Asn Ile Val Gly Val Ile Leu Leu
 755 760 765
 Gln Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu
 770 775 780
 Asn Val Val Phe Val Thr Cys Glu Tyr Asp Asp Thr Val Thr Asp Val
 785 790 795 800
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 Glu Pro Asn Ser Thr Gly Asn Pro Phe Gln Gln Lys Leu Gln Asn Glu
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 Phe Ser Leu Pro Ser Asp Ile Glu Met Pro Leu Gln Met Ser Lys Gln
 850 855 860
 Lys Ser Lys Ser Gly Val Asn Gly Ser Phe Ala Ala Leu Glu Leu Ser
 865 870 875 880
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 900 905 910
 Val Pro Ala Ala Phe Arg Val Pro Ser Gly Ala Val Ile Pro Phe Gly
 915 920 925
 Ser Met Glu Asp Ala Leu Lys Lys Ser Gly Ser Leu Glu Ser Phe Thr
 930 935 940

Ser Leu Leu Glu Lys Ile Glu Thr Ala Lys Val Glu Asn Gly Glu Val
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 Asp Ser Leu Ala Leu Glu Leu Gln Ala Ile Ile Ser His Leu Ser Pro
 965 970 975
 Pro Glu Glu Thr Ile Ile Phe Leu Lys Arg Ile Phe Pro Gln Asp Val
 980 985 990
 Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu Asp Leu Ala Gly Met
 995 1000 1005
 Ser Ala Ala Gly Leu Tyr Asp Ser Ile Pro Asn Val Ser Leu Met
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 Asp Pro Cys Ala Phe Gly Ala Ala Val Gly Lys Val Trp Ala Ser
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 1040 1045 1050
 Tyr Gln Arg Asp Ala Thr Met Ala Val Leu Val Gln Glu Ile Leu
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 Gln Pro Asp Leu Ser Phe Val Leu His Thr Val Cys Pro Ala Asp
 1070 1075 1080
 His Asp Pro Lys Val Val Gln Ala Glu Val Ala Pro Gly Leu Gly
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 Glu Thr Leu Ala Ser Gly Thr Arg Gly Thr Pro Trp Arg Leu Ser
 1100 1105 1110
 Cys Asn Lys Phe Asp Gly Lys Val Ala Thr Leu Ala Phe Ser Asn
 1115 1120 1125
 Phe Ser Glu Glu Met Val Val His Asn Ser Gly Pro Ala Asn Gly
 1130 1135 1140
 Glu Val Ile Arg Leu Thr Val Asp Tyr Ser Lys Lys Pro Leu Ser
 1145 1150 1155
 Val Asp Thr Thr Phe Arg Lys Gln Phe Gly Gln Arg Leu Ala Ala
 1160 1165 1170
 Ile Gly Gln Tyr Leu Glu Gln Lys Phe Gly Ser Ala Gln Asp Val
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Glu Gly Cys Leu Val Gly Lys Asp Ile Phe Ile Val Gln Ser Arg
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Pro Gln Pro
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27

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21

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25

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 tac 63

<210> 23
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 gcctgca 67

<210> 24
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 <213> Artificial Sequence

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<210> 25
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<400> 25

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50